

Protein Isoforms

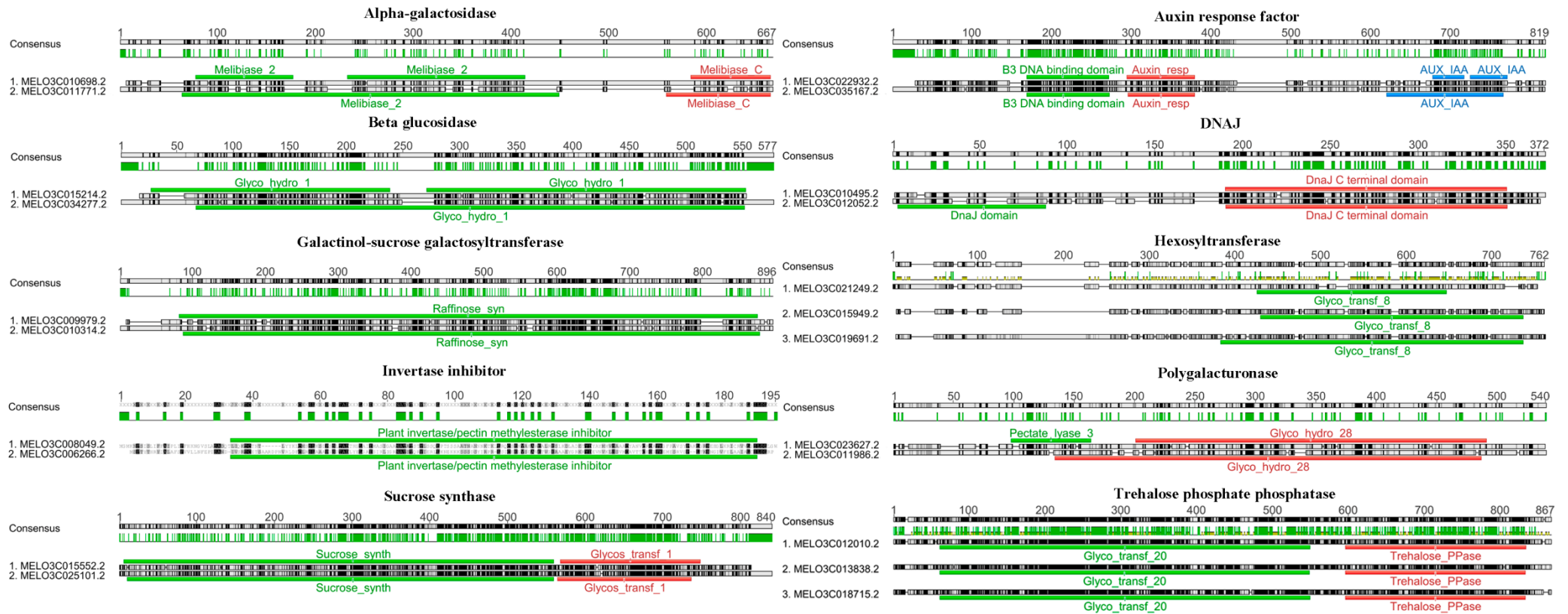


Figure S11 Alignment of proteins isoforms related with sugar metabolism or associated pathways. The domains were detected by Pfam database (<https://pfam.xfam.org/>) and the amino acid sequences were aligned by MUSCLE algorithm.

Protein isoform sequences alignment using MUSCLE algorithm and similarity percentage (<http://imed.med.ucm.es/Tools/sias.html> software). (*)as sequências idênticas na posição; (:) substituições conservativas; (.)substituições semi-conservativas.

1) Alpha galactosidase

```

MEL03C010698.2 -----MKNVCFSLFFSFGLLF-----NWVSSQTGPERAL-----
MEL03C011771.2 MALSPSPSPVMVLLYFVLSWTFLLGGNGNGVAVAGASRSTALRFAAEFDSVSSRRVLLNN
      * . * . * : . *      * * : . . : **
MEL03C010698.2 -----PPRGWNSYDSFSWIIEEEFLNNVE-IVANKLKSKGYEYIVDYLWYRKKVPGAY
MEL03C011771.2 GLALTPPMGWNSWNHFQCNLNENLIKETADAMVSSGLAALGYEYINLDDCW-----AE
      ** * * * * : * . : * : : : : * : * : * * * : * *      *

MEL03C010698.2 TDSLGFVDIDEWGRMAPDVRWPSSQGGKGFSEVAKKVHAMGLKFGIHMVRGISTQAVNA
MEL03C011771.2 LDR-----DSKGNLVAKASTFPS-----GIKALADYVHRKGLKLGIIY-----
      *      * . . . . . : **      * : . * . * * * * * :

MEL03C010698.2 NTPILDISKGDAYVESGKKWLASDIGIKSRACGWMHNGFMSVNVKSGAGKAFRLRSLYQQY
MEL03C011771.2 -----SDAGIQTCCKMPGSLGNEEQDA-----KTF
      . * * : : : . * . . . . * : . . .      : :

MEL03C010698.2 ADWGVDFVKHD-CVFGDDLDLDEITFVSDVLKQLNSTIVYSLSPGTSATPAMAKAVSGLA
MEL03C011771.2 ASWGIDYLKYDNCENTGTSPKERYPKMTKALQQSGRPILFSLCEWQEDPATWAVNVG--
      * . * * : * : * * . : . : . . * : * . * : * * . * * . *

MEL03C010698.2 NMYRITGDDWDTWNDIVSHFDVTRDFATANMIGTAGLLGKSWPDLMLPLGWLTDPGSNN
MEL03C011771.2 NSWRTTSDIQDNWISMTTIADQNDKAWASYAKPG-----GWNDPDMLEVG-----N
      * : * * . * . * . : : : * . : * : *      * * * * * : *

MEL03C010698.2 GPHRTTNLNIQRTQMTLWSISKSPIMFGDLRNIDNTTFSIITNPTLLEINSFSSNNM
MEL03C011771.2 G-----GMTTAEYRSHFSIWALAKAPLLIGCDIRSDNITMKLLSNKEVIAVN-----
      *      . . . * * : : : : * : : * : * * : * * : * : : * : : *

MEL03C010698.2 EFLKIASTNFRKRVKWHSRGLEASASPIGLTKCAYSDDTGWITKSVDQGLEKICWKAN
MEL03C011771.2 -----QDKLGV-----
      .      * * :

MEL03C010698.2 PEHEYQTPFCLYKGRSRVAIDKEAATHRDQVELLSFSTSSVEVCLDATPKRKHSSAIMR
MEL03C011771.2 -----QGKKV-----
      . * . *

MEL03C010698.2 GSFFPCKRHENQKWDLYANGTLANHNSGHCAIVKYKQAKAIPTGVRSWVATGRGGEVYVA
MEL03C011771.2 -----YKYGDLE-----VWAGPLSGKRVAVV
      * * *      * . . . * * * .

MEL03C010698.2 FFNLNNVKTVISAKISDLAALPGKLLGNPNSCKYREEWVGDFGLVSDLIAAPVESHGSA
MEL03C011771.2 LWNRLWRANITASWSDIGLC-----SSTTVTARDLWQHSS-QVVQHHLTAQVDSHDCK
      : * . : : * : * . * * : . . . . . : * : * . . : * . : * * * .

MEL03C010698.2 LFIINCS
MEL03C011771.2 MFVLTPLH
      : * : .
    
```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```

MEL03C010698.2 100%
MEL03C011771.2 29.11%      100%
                MEL03C010698.2 MEL03C011771.2
    
```

2) Auxin response factor

```

MEL03C022932.2 -----MSFSAASNLPSSGGPHSGPSSDALYRELWHACA
MEL03C035167.2 MEIDLNQTA SEVGKNAYCYGNCEEGLCNCLSSSTSSCSSNSSTPVSSSTYLELWHACA
      . * : : : . * . . . * * * : * * * * *

MEL03C022932.2 GPLVTLPRQDERVYFYPQGHMEQLEASMHQGLEQQMPSFNLPKILCKVNVVLAESDT
MEL03C035167.2 GPLTSLPKKGNVVVYFYPQGHLEQISSASPFS-PEMERTFDLQPQLICRVINVHLLANKEN
      * * * : * * : : : * * * * * : * : * : * * * * * * * : : .

MEL03C022932.2 DEVYAQITLLPESNQNEVTSPDPPLPE-----PTRCNVHSFCKTLTASDTS
MEL03C035167.2 DEVYTQLTLRPLPELLGTGVAGKELEELALNGADGDGSGGSPTRSTPHMFCKTLTASDTS
      * * * : * * * * : . . . * *      * * * . * * * * * * * *

MEL03C022932.2 THGGFSLRRHADDCPLPLDMSQQPPWQELVATDLHGSQWHRFRHIFRGQPRRLLTTGWS
    
```



```

: *:*:*:*:* * * : * * * * :*..*** *..* . :***** .**:.
MEL03C015214.2 KRLPKFKDDEIVLVKGSYDFLGINYYTANYAKNPNVD-PNKPSQVTDADAVDSTDRDGV
MEL03C034277.2 SQLPSFSKTEKSIKGLDYICVNHYYTLYTKDCLHSPCSNGGDRPIKGFLLDTTGYRDSV
..**.*. * :.*** *:. :*.** :*:. : * .. ... *:. **.*

MEL03C015214.2 SIGPKVRKDSWLAVYPQGLKDLMIHIKKYYRDPPIYITENGY--LDYDCPNVEKLIKDEG
MEL03C034277.2 SIGDPTGVDRFFV-PRGLEKIINYIRQYPNPIVVTENGYSMPPSDGKTLEDIINDTK
*** . * :.* *.***:. :*. : * : * * :***** * ..*:*:*

MEL03C015214.2 RVKYHQHLIKLHESIKAEVNIKGYFAWLLDDFEWSRGYTMRFGITYVDFKHKTLEIRIP
MEL03C034277.2 RVNFHKNYLASLVRAMRNGADVRYFVWSLMDNFEWIDGFTTRFGLWYVDF--QTLERRP
*:*:*:*:* * :. :. :.***.*:*:*** *:* ***: **** :**** *

MEL03C015214.2 KHSARWFNFHFLHT-----
MEL03C034277.2 KLSAHWFASFLLGGNLHQLTKSSSIIDKKNFRSLTYD
* **.* * *

```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```

MEL03C015214.2 100%
MEL03C034277.2 49.31%      100%
MEL03C015214.2 MEL03C034277.2

```

4) DNAJ

```

MEL03C010495.2 -MVDLPQALGISFR---NFCKSYKSFKKWHSKVKNSKKTNDNVDTKHDDATSDAIHN
MEL03C012052.2 MGVDYYNVLKVNANEDDLKRSYKRLAMKWHPD-----KNPCNKKEAEA-----
* * :.* :. . :. :.*** : **.. * :.* :.*

MEL03C010495.2 HSPSKDHEEIKKKEGPRPTTTTRGVHSFRYGGRLRENDTTSFRPRSVDGSGYTLRNAS
MEL03C012052.2 -----KFKQISEAYDVLSDAKKRQIYDL-YGEEALKSADFVP--PPNSNPSFSYVPRDAD
...*:.*. . . :.* :.*** ** :*.. * .. * . :.*** * :.*.*

MEL03C010495.2 RRQNPASTSSSLFRSVSRSSNESMPSRVSSGRRSIDSISSSPVLKSGSRRSTTPIMFS
MEL03C012052.2 -----DIFAEFFGGAG-----SGKSRGFRGELFKNGKAEAVKQTNR-----
. :.* ... * * * * . :. . . . :.*

MEL03C010495.2 NSSGVLKAAPIEKQLECTLEELCFGCMKKIKIMDIIMDR--QAMEEETLTIKVKGWRK
MEL03C012052.2 -----KAPPIESKLLCSLEELYKGSRRKMRIISRTVADEFKPKTVDEVLKIDIKPGWK
**.***.* *.*** * . * :.* : * :. :.*.*:****.*

MEL03C010495.2 GTKITFEGGTNERAGSYPADTSFVIAEKRHSYFKREGDDLELMVEIPLLKALTGTCTIPV
MEL03C012052.2 GTKITFP-EKGNQEPGVAPADLIFIIDEKPHPVFERDGNLNVNQKMSLLEALTGKTLNI
***** .**.* * ** *.* * * . :.*:*:* : :.***:**** * :

MEL03C010495.2 PLLGGETMSLEIHEVSPGYEKLIQGGMPKLDPNNRGNLIVKFFVHFPTQLTPQQRSD
MEL03C012052.2 TTLDGRDLT-TVTDIVKPGYEVVFQNEGMPISKEPNKGNLRIKFDIVFPSKLTFEQKSD
.*.* :. : :.*.*** :*:* ** *.*.* ** * : *.* ** *.* **

MEL03C010495.2 VCRILEASHYPS
MEL03C012052.2 LRRALGGSD---
: * * .*

```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```

MEL03C010495.2 100%
MEL03C012052.2 45.39%      100%
MEL03C010495.2 MEL03C012052.2

```

5) Galactinol-sucrose galactosyltransferase

```

MEL03C010314.2 MALNRWLFNSPVLTTINTSRFFLSSSPWIVSDFNLVTTKKEHSVSDLRICTFTRSRHSS
MEL03C023110.2 -----
MEL03C009979.2 -----

MEL03C010314.2 VKAFKVNLLKGRELESELKAKEMTIKPAVRISDGKLVKDRITLTGVPDNIATSGSSSG
MEL03C023110.2 -----MTVTPKISVNDGNL VVHGKILTGVPDNIIVLTPGSGLG
MEL03C009979.2 ----MAPSLKNGGSNVVDFDGLNDMSSPFAIDGSDFTVDGHLFLSDVPENIVASPSPTY
:.. . :.*** :*:* **.*: :. . .

```

MEL03C010314.2 P-----VEGVFLGAVFEEEQSRQVSLGTLRDVRFMACFRFLWMAQKMGDKGKEIPLE
MEL03C023110.2 L-----VAGAFIGATASNSKSLHVFVPGVLEGTFLCCFRFLWMTQRMGTSGRDIPFE
MEL03C009979.2 IDKSPVSVGCFVGFDASEPDSRHVVSIGLKDIFRMSIFRFKVVWTTTHWVGRNGDLESE
::* .:.*:*.:.*. *.. **:. **:*:* *:*:* *:*:* *:*:*

MEL03C010314.2 TQFLLLETKDGSHLESDDGNEENQIYTVFLPLIEGFRACIQGNGQDELELCEESGDVD
MEL03C023110.2 TQFLLMESKNGDGEDPDNSS-----TIYTVFLPLLEGQFRAALQGNEKNEMEICLESNDT
MEL03C009979.2 TQIVILEKSDSGRP-----YVLLLPIVEGPFRTSIQPGDDDFVDCVESGSSK
::*:*..... *:*:*:*:* *:*:*:* .:.*:*:*:*

MEL03C010314.2 TKASSFTHSLFIHAGTDPFDAISDAMKAVKHLNTRFLRHEKKLPAIVDYFGWCTWDAFY
MEL03C023110.2 VETNQGLSLVYMHAGTNPFEVITQAVKAVEKHTQTFHLHREKKLPSFLDWFGWCTWDAFY
MEL03C009979.2 VVDASFRSVLYLHAGDDPFALVKEAMKIVRTHLGTFRLLLEKTPPGIVDKFGWCTWDAFY
. . ::*:* *:* .:.*:* *.* ** .:.*.*:* *****

MEL03C010314.2 HEVTQDGV EAGLES LTAGGVPPKFVIIDDGWQSVGGDPQEEKEEGD----EKQPKQAPLL
MEL03C023110.2 TDVTAEGVVEGLKSLSEGGAPPKFLIIDDGWQQIEAKPKDADCVVQ----EGAQFASRLS
MEL03C009979.2 LTVHPQGVIEGVKHLVDGGCPPGLVLIIDDGWQSIGHSDPITKEGMNQTVAGEQMPCRLL
* .:* *:*:* * * * * :*:*****.: * . *

MEL03C010314.2 RLTAIRENSKFQK-----EEDPTEGIKNIVNIAKNKYG-LKYVYVWHAITGYWGGVRTGV
MEL03C023110.2 GIKENHKFKQNGN-----NYDQVPLKVVVDDAKKQHK-VKFVYAWHALAGYWGGVKPAS
MEL03C009979.2 KFQENYKFRDYVNPKATGSGDQKGMKAFIDELKGEFKTVEYVYVWHALCGYWGGLRPQV
: : . : . * *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 KDMEYGSMMQYPKVKSGVFENEPWKNDALALQGLMNPKNVYKFYNELHSYLASAGI
MEL03C023110.2 PGMEHYDSALAYPVQSPGMLGNQPDIVVDSLAVHIGLHVHPKVFNFYNELHSYLASCGI
MEL03C009979.2 PGLPEAR--VIQPVLSPLQMTMEDLAVDKIVLHKVGLVPEKAEMEYGLHSHLEKVGI
.: . : * *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 DGVKVDAQSILETLGAGLGGRVELTRQYHQALDASVARNFPDNGIACMSHHTDAVYC-A
MEL03C023110.2 DGVKVDVQNIETLGAHGGRVTLTRSYHQALEASIAARNFSDNGCIACMCHNTDSLYS-A
MEL03C009979.2 DGVKIDVIHLLEMLCEDYGRVLDLAKAYKAMTKSINKHFKGNVGIASMEHCNDFMFLGT
***:*:* .:.* * * . *** *:* *:*:* *:* *:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 KQTAVVRASDDFYPRDPVS-----HTIHIAAVAYNTVFLGEIMLPDWMFHSLSHAA
MEL03C023110.2 KQTAVVRASDDYYPDPAS-----HTIHISSVAYNSLFLGEMQPDWDMFHSLSHPTA
MEL03C009979.2 EAISLGRVGDWFCTDPSGDPNGTFLWLGCHMVHCAYNSLWGMNF IHPDWMFQSTHPCA
: : *:*:*:* * * . : * * *:*:*:*:*:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 EYHASARAISGGPVVSDAPGKHNFFELRLKLVLPDGSVLRATLPGRPTRDCLFSDPARDG
MEL03C023110.2 EYHGAARAIGGCAIYVSDKPGNHNFDLKKLVLDPDGSVLRALPGRPTRDSLFPNDPARDG
MEL03C009979.2 AFHAASRAISGGPIYVSDSVGKHNFDLKKLVLDPDGSILRSEYALPTRDCLFADPLHNG
::*:* * .:***** *:*:*:*:*:*:*:*:*:*:*:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 VSLLKIWNLNKFTGVVGIYNCQGAAWNSQERKNTFHDTNSDAITGVYKGRDVHAIS-EVA
MEL03C023110.2 TSLKKIWNMKNKSGVGVFNCGAGWCRIKTKTRIHDSPGLTTSVRAAGVDVAIS-QVA
MEL03C009979.2 ETMLKIWNLNKFTGVIGAFNCQGGGWCRETRRNQCFQYSKRVTSKTNPKDIEHWSGENP
*:*****:* *:*:* *:*:* * * :* . . . * * . *:* * * . *

MEL03C010314.2 ADPNWNGDCAFYRHRSGDLITLPYNSALPVSLKVLFEFIFTITPIKVLAPG-FSFAPLGL
MEL03C023110.2 G-ADWKGDTIVYAYRSGDLIRLPKASVPVTLKVEYDLFHISPLKDIASN-ISFAPIGL
MEL03C009979.2 ISIEGVKTFVLYLQAKKLIISKPSQDLIALDPFEFELITVSPVTTLTQTSLHFAPIGL
: * :* : * * . : : * . *:*:*:* *:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 IDMYNSGGAIEGLKYEYKGGAELEVDGTSEGTEAAGERAENRSEELVGIHVLEVKGCGK
MEL03C023110.2 LDMFNTGGAVEQVNVQVVEIPEFDGEVASELTCSLPD-----DRPPTATITMKARGCGR
MEL03C009979.2 VNMLNTGGAIQSVYDIDD-----LSSVEIGVKGCGE
:* *:*:*:*: .: . : . : . : *:* *:* *:* *:* *:* *:* *:* *:* *:* *:*

MEL03C010314.2 FGAYSSAKPRRCIVDSSVVEFGYDSEGLLTLGIDKLPEDLKYHDIKIEL-
MEL03C023110.2 FGLYSSQRPLKCSVDKVDVDFVYDEVTLGLVTFEIPTEEMRWNIIEIQV--
MEL03C009979.2 MRVFASKKPRACRIDGEDVGFKYDQDQ-MVVVQVPWPVDSGSGGISVIEYLF
: : *

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

MEL03C010314.2 100%
MEL03C023110.2 53.23% 100%
MEL03C009979.2 37.24% 37.69% 100%

6) Hexosyltransferase

```

MEL03C021249.2 MAFFTRKQPLLNLSLPQSHSPSSSSSSSSSSSSSSSSSSSSQNLKFKINKLRRSRSSSLILFFIF
MEL03C015949.2 ---MRRRPPDFRRPARRRLSNA-----FWWT
MEL03C019691.2 --MASKRGLLSATAAHRARAGGSRIP-----LLLIVIF
    . . . . .
MEL03C021249.2 LFFILLLCFLFLISFT-----LLSSNSNSNSTITNS--LREIPTVIDSEFQETI-----
MEL03C015949.2 LCFVAVLLFVF-----ILTKGPQ-----IESTRPVLARR-----
MEL03C019691.2 FFFLSPVLFFFGRGFRAADLEIISGSGQQDVGWRERIALHQFKSLFSKEVIDVIAASTN
    : * : * . * : : . . . : : : . : :
MEL03C021249.2 KIGLINISTDDKDEIHDTLHLLGLIENRRSR-----
MEL03C015949.2 -----SYRHEGIMEGLNITEEMLNPSI-----
MEL03C019691.2 DMGPLYSDHFRKNNFSASWIKNGQEVTPDGIPERNRMVVDLGEKSDSEEVKLMDSSQS
    : : : : . .
MEL03C021249.2 -----IETVTVDFDRIEKEFE
MEL03C015949.2 -----
MEL03C019691.2 TDSPTKQARRLHVQQLREKXREKRAAQLLQDDDLIKLENAAIERSKSVDTSVLGKYSI

MEL03C021249.2 W-----ERLFPWEIDEDEKYKSSPKCPNIPMPKTEDYSDLNIVVLRIPCKRGI
MEL03C015949.2 -----ARQLSDQISLAKAFVVIKAKESS-----NLQFAWELSA---QIRNSQIL
MEL03C019691.2 WRKENENENTDATVRLMRDQIMARAYLGIAMKN---KLDLYHELQT---RLKESQRA
    * : : : : : . * . : : * . : : . .
MEL03C021249.2 LTSRDVFRQLQANLAAARVAVASGWVEEIIYRTVYVVFLGECGAMREIFRCDDLVIKDDRT
MEL03C015949.2 LSSAATRRLAQITEAETAIRD--MALLLYQAQQLHY--DSATM--IMRLKAKIQTLDLDEQ
MEL03C019691.2 LGFAST--DADLNRSAPDK-IKS--MGQILSKAKEQLY--DCKLV--TGKLRAMLQSADEE
    * . . : : . : : : : : : : : . : . *
MEL03C021249.2 VENVWVKPEIKRLKQKILLPFGSCQLAPVYARTGREVWRHFMLQKPPKTNSTTTTHYHKP
MEL03C015949.2 MSSVSDKSSKYGQIAAEVPKSLYC---LGVRLTTEWFKNLNLQKKLSEKQIDMKLKD
MEL03C019691.2 VRGLKKQSTFLSQAAKTIPNGIHC---LSLRLTID-YHLLPLEKRFPRSE---NLEN
    : : . . : : : * : * : : : * : * . :
MEL03C021249.2 KQAYVTILHSSEAYVCGAIALAQSLLQTNTSKDLILLADNSISPNSIQALKDAGWVYMRI
MEL03C015949.2 NDLYHFCVFSNLIATSVVNSTALNSKNPDRIVFHLVTDDEVNYAAMKA-----WFSM--
MEL03C019691.2 PNLHYHALFSDNVLAAASVVVNSTIMNAEDPSKHVFLVTDKLNFGAMNM-----WFLS--
    : * : * . : . . : : : : . . . : * . : : : : * :
MEL03C021249.2 DRIRSPFSEKGSYNEWNY-----SKLRIWQLTMY-----DKIVFIDA
MEL03C015949.2 NNFRRVTVDVQMFEDFSWLNASYVPVLKQLQSDTQNYYSFGNGGDSR-----TPIKFRNP
MEL03C019691.2 NPPGKATIHVENVDFKWLNSSYCPVLRQLESAAMKEYYFKAGHPPTLSSGASNLKYRNP
    : : : : : : * * : : :
MEL03C021249.2 DLLVLKIDQFFALPQLSAAANNKMRFNNGVMIVEPSACLFEELMEKSFELKSYNGGDQG
MEL03C015949.2 KYLSMLNHLRFY-IPVFPALKKVVFLDDDDVVVQRDVSGLFS-----IDLNGNVNG
MEL03C019691.2 KYLSMLNHLRFY-LPQVYPKLEKILFLDDDDIVVQKDLTGLWD-----VDLHGKVNK
    . * : * . * : * : : . : : : : : : : : * . . : * : *
MEL03C021249.2 FLNEVFTWVHRLPSRVNLYKIFLKENSENDSDGTPYAIHYLGLKPWMCYKDYDCNWDMED
MEL03C015949.2 AVETCMETFHRYHKYLNYSHPLIREHFDPDACGWAFGMNVFDLVEW---RKRNVT---GI
MEL03C019691.2 AVETCGESFHRFDKYLNFSPHPIARKFDPNACGWAYGMNMFDLKEW---KKRDIT---GI
    : : : * . * : : : : : : : : : : * * . . .
MEL03C021249.2 HQIFASDSAHAHAKWQIYESMPTELQHFQGLTKKMDSRIRKWRRIARNNSTFADAH-----
MEL03C015949.2 YHYWQEKNDVRLWKL-GTLPPLGTYFGLTEPLD---PSWHVLGLGY-TNVDSQLIEKG
MEL03C019691.2 YHKWQNLNEERLLWKL-GTLPPLGTYFGLTEPLD---KSWHVLGLGNPSIDKSEIENA
    : : . . * : : * * * * : * . * . . . *
MEL03C021249.2 -----W-KIKITD--PRRHRLMDDHAP-----
MEL03C015949.2 AVLHFNKSPWLKIGIEKYKPLWEKYVDYTHPLQSCNFH-
MEL03C019691.2 AVIHYNGNMKPWLELAMTKYRGYWTYIKYNHPYLRQCKLNE
    * : : . . . . *

```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

MEL03C015949.2	100%		
MEL03C019691.2	56.17%	100%	
MEL03C021249.2	18.72%	18.72%	100%
	MEL03C015949.2	MEL03C019691.2	MEL03C021249.2

7) Invertase inhibitor

```
MEL03C008049.2 --MGMKNFSISLIFFAIPLIFFHKNVSLASADQTLIQTCTNTLYYKLCMSSLKSDPSS
MEL03C006266.2 MSFTYTHRYIALAFSFVLLNFEPISANDIVSRTCETSAARDPNVRLDFCLRSLAAAPGS
      : .: *:* * : *:* . . . : . : .: .:* * : *
      :

MEL03C008049.2 LTADTKGLAIIMASIGAANATATSTYLSSQLPTSSAATNANNKTKLLRQCSEKYAFAA
MEL03C006266.2 DTADLYELGAISIRLIGNATSTQRYIERLLKNEKKKSSSDSYIRPLS-DCEELYSDAV
      *** * . * : . ***.* * . * . . . . : . : .:* *:* * : *
      :

MEL03C008049.2 EALRESLKDLADETYDYAYMHVSAADYANVCRDAFKGFPVAVSYPAKLRREEGLKRICR
MEL03C006266.2 ETVGEEAAEYGRKRYDEVNVKLSVMDAVTTCEDGFKEMESRVSP--LTKRNGDVFELAA
      *:: * : . : * . : : : * . * . . * . * . * : : * * * : . : .
      :

MEL03C008049.2 VVLGILDLLGW
MEL03C006266.2 IALCILDLRP-
      : . * ****
      :
```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```
MEL03C008049.2 100%
MEL03C006266.2 32.08%          100%
                  MEL03C008049.2 MEL03C006266.2
```

8) Polygalacturonase

```
MEL03C011986.2 MPTKMASLFSFINSNLFSLIALIQTITLVISSNNSTEMDKLFLLSLLGLLIIAYGVSGTF
MEL03C023627.2 MP--MEKLY---KNPIKAQVMKMVILGVIMAAALMDEVE-----GRRGKV
      ** * .:* : . : .: : : : : : * : : * * .
      :

MEL03C011986.2 VSDSDIDMIEELESFDIEEEDDDVVYSYTPAWRSERGSKILMNVDSDAVDGDVDDTM
MEL03C023627.2 KKGKKAKI---LENGIE-----YGAINCRAHTS-----ITEFGGVDGVTSNTK
      . . . . : . : * . * * * * * * * * * * * * * * * * * * * * * *
      :

MEL03C011986.2 AFRKAWETA---CSTSKSVLLVPKEKRYLVNATTFKGPCKDGMVIQIEGTIVAPDEPELW
MEL03C023627.2 AFQAAVERLQYANDGGAQLVYPAG--RWLTG--SFNLTSHFTLFLHQDAVLLASQDPNEW
      ** . * * . . . : * * * * * * * * * * * * * * * * * * * * *
      :

MEL03C011986.2 D-----PKFPR-----QWLEF---TKLNAATFQG--DGVIDSGGEKWWAESCKKNKSRP
MEL03C023627.2 PVVEPLPSYGHGRDTSGGRYISLIFGTNLTDVVITGNNGTIDGQGDWRW--QLFHQGLKY
      * . : . . . : : * : * . . . * : * * * * * * * * * * * * *
      :

MEL03C011986.2 CKGAPTAFTIDSSNIRVKGLTIQNSQQMHFTIARSETVRITEVRSAPGDSPTDGIHI
MEL03C023627.2 TR--PYLIELMYSRDIQISSLTLLNSPAWNVHPVYSSNILIQGITIIAPVRSPTDGINP
      . * : : * : * . . * * * * * * * * * * * * * * * * * * * * *
      :

MEL03C011986.2 TQSTNVVQNSKISTGDDCISIVNA--SSGIK-----MKGISCGPGHGISIGSLGK
MEL03C023627.2 DSCTNVRIEDCYIVSGDDCVAVKSGWDEYGIRFLPTKQLVRRRLTCISPTS AVI--ALGS
      . . * * * * * * * * * * * * * * * * * * * * * * * * * * *
      :

MEL03C011986.2 DNSTGIVTKVVLDTAFLRETTNGVRIKTTWQGGSGYVRSVRFENVRMEDVENPIIDQFYC
MEL03C023627.2 EMSGGI-QDVRAEDIVAINSESGVRIKTGIGRGGYVKDIYVRRMTMHTMKWAFWMTGDYG
      : * * * . * : . : . : * * * * * * * * * * * * * * * * * *
      :

MEL03C011986.2 DSPTTCETQTSAVKISQIMYRNISGTTTSKNAMKFCSDSVPCSNIIILSNVLEKTDGTV
MEL03C023627.2 SHADKNYDPHALPVIQGINYRDMV-VENATMAARLEGISGDTFTDICSINVITGLAPKAK
      . . . : * . * * * : . . . * : . . . : * * * * * : : :
      :

MEL03C011986.2 ET--YCHAAQFGYGVIVHPSADCLTSSDNNFAALDQ--TQVLELETVQLPTEQHIVHTEL
MEL03C023627.2 KQPWTC TDVEGITSQVTPPPCDLLPDQGEKITTCKFPEDNLPIDAVQLKKCSYQFSHA-
      : * . : * : . * . * * . . . : : : : * : * * * * . . .
      :
```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```
MEL03C011986.2 100%
MEL03C023627.2 26.97%          100%
                  MEL03C011986.2 MEL03C023627.2
```

9) Sucrose synthase

```
MEL03C015552.2 MAERVLNRVH--SLRERLDELIAQRNEILGLLSKIEAKGKILQHHELIAEFETIPEE-
MEL03C025101.2 MASLVVNHNGESIGDGIIVEALKQNQNYMKTFCGKGFVEKGNRSLKKKELMEEMELVIDDK
```

```

**.*.*. : * : : *.* :.* : :.* ** : *::*: *.* : :
MEL03C015552.2 -NRKKLADGAFGEVLRSTQESIVLPPWVALAVRPRPGVWEYIKVNVHALVVEELQVSEYL
MEL03C025101.2 IERNRVMEGILGHMLTSTQVAIVIPPYVAFAIRPEPGCWEYVKVSSLDLSQLSTSTFEL
.*.: : * : * : * ** .**.*.*.*.* ** * **.*.*. * :.* : *.*
MEL03C015552.2 RFKEELVDGS-SNGNFVLELDFEPFNASFPRPTLSKSIGNGVEFLNRHLSAKLFHGKESM
MEL03C025101.2 KLKEMIYDEEWANDENALEVDFGAIFFTTPHLSLPSISIGDGLSYTTKFLTSLKSGKLENL
.*.* : * . :.* : **.* * : : * . :.*.*.*.* :. . :.*.* * :.
MEL03C015552.2 QPLDLFLRVHCYKGTMMLNDRIQTLNLFQHVLRKAE EYLVTLAPDTPYSDFANKFQEIG
MEL03C025101.2 QPLVDYLLSLDYQGEKLMINETLNTPSKLMALILADIFLSVLPHTPYDDFHLKQKQW
**.*.* * :.*.:.*.* :.* . :.* * : :.* * **.*.* * : : *
MEL03C015552.2 LERGWGDAERVLEMIQLLLDLLLEAPDPCTFEKFLGRIPMVFNVVILSPHGYFAQDNVLG
MEL03C025101.2 FERGWGDCAGRVKETMRCLSEIFQAYDPIQMEKFFSR LPTTFNVVILSPHGYFGQAGVLG
:***** * ** * :. * : :.* ** :***.:.* .*****.* **
MEL03C015552.2 YPDTGGQVVYILDQVRALEHEMLQRKQGLDITPRILIIITRLLPDAVGTCTQRLEKVF
MEL03C025101.2 LPDTGGQVVYILDQVKAMEEELLRKQKGLNFKPQIIITRLIPDAKGTCKNQEIEPVI
*****.*.*.*.* *****.:.*.*.*.*.* **.*.*.*.*
MEL03C015552.2 GTEHSHILRVFPRNEKGIWRKISRFEVWPYLETYTEDVAQELTKELQKPDLIIGNYSD
MEL03C025101.2 GTNYSKIVRVPFKTENGILHRVWSRFDIYPYLEKFAQDASDKILELMEAKPDLIIGNYTD
*.:.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 GNIVASLLAHKLGVTQCTIAHALEKTKYPSDSIYWKRFDEKYHFSSQFTADLIAMNHTDF
MEL03C025101.2 GNLVSLMASRLGVTQGTIAHALEKTKYEDSDLKWKELDSKYHFSCQFTADLIAMNATDF
*.:***.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 IITSTFQEIAGSKDTVGQYESHAF TLPGLYRVVHGIDVDPKFNIVSPGADMSIYFPYT
MEL03C025101.2 VIASTFQEIAGSKEKPGQYESHAF TLPGLCRVVSGINVDPKFNIAAPGADQSVYFPYT
:.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 ETEKRLTSFHPEIEELLYSEVENEHL CVLKDRSKPIIFTMARLDRVKNITGLVEYWGKN
MEL03C025101.2 AKELRFASFQPAIEELLFSKVENNEHIGYLADRKKPIIFSMARLDVVKNTGLVEVFGKN
.* :.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 NRLREL VNLVVVAG--DRRKEKDNEEKAEMEKMYNLIKTYNLNGQFRWISAQMNRVRNG
MEL03C025101.2 EKLRNLVNLVVVGGFDPKSK-SKDREEMAEIRKMHELIDKYQLKQIRWIAAQTRRRNG
:.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 ELYRCIADTKGAFVQPAVYEAFLTVVEAMTCGLPTFATCNGGPAEIIIVDGKSGFHIDPY
MEL03C025101.2 ELYRCIADTKGAFVQPALYEAFLTVIEAMNCGLPATNQGGAPEIIIVDGVSQFIDPN
*****.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 RGDRAAEILVDFFEKSKEDPTHWDKISQAGLKRIYKYTWQIYSERLLTLTGYYGFWKHV
MEL03C025101.2 NGENSSQKIANF FEKCKNDPTYWNEISNHGLQRINECYTWKIYAKKVLNMGSTYTFWKQV
.* : : : :.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*
MEL03C015552.2 SNLDRLESRRYLEMFYALKYRKLADSVPPAVDE-----
MEL03C025101.2 NKNQKQAKDRYIQMFYNLLFKNLVKTVPVVDENPHPGNPQLPQVSKRTQSRIQKFFGAP
.: . . *.:*** * :.*.:** .***

```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```

MEL03C015552.2 100%
MEL03C025101.2 65.5% 100%
MEL03C015552.2 MEL03C025101.2

```

10) Trehalose phosphate synthase

```

MEL03C013838.2 MVSRSYSNLLELASGGCSPTFGLGRERKRLPRVATVAGVLSLEDDSCNSTGSDAPSSVA
MEL03C018715.2 MISRSYTNLLDLASG---NFPAMEVKKRFRPVMTVPGNVAELDDQAYSVTSENSSIS
MEL03C012010.2 MASRSTANFLDLASG---DLLDVPRTPKSLPRVMTAPGIISELDYDGSNDGDSSE-SVVY
* ** * :.*.*.*.* * :*** *.* * :*** . . * : **
MEL03C013838.2 QDRMIIVGNQLPIRANRNNEN-GDWEFSMDEDSLLLQLKDGLGEDVEVIYIGCLREEVDP
MEL03C018715.2 SDRMIIVANQLPLRAKREDDNSWSFSWNEDSLLLQLKDGLPEDMEILYVGSCLKVDIQPE
MEL03C012010.2 RERKIIIVANMLPLHAKKDGQSGKWCFLDEDSILLQLKNGFSPEMEVIYIGSLKVEIDPS
.* **.* **.*.: : . . * ** :***.*.*.*.* : :.*.*.*.* : :.*
MEL03C013838.2 EQDDVAQTLLDRFKCVPTFLPPELFSKFYHGFCQHLWPLFHYMLPLSPDLGGRFDRSLW

```



```

MEL03C018715.2 EQDEVSQLLERFRCIPAF LPPHILEKFYDGFCKRHLWPLFHYMLPYSADQKGRFDRSMW
MEL03C012010.2 EQEEVAQKLFDFNFCVPTFLPHDLQKNFYIGFCKQLWPLFHYMLPMCPEHGDRFDRQLW
**:.*** *::.*.*:.*.*** ..:.* ***:.*:***** ..: .***.*

MEL03C013838.2 QAYLSVNKIFADKVMESISDFFVWVHDYHLMVLPFLRKRFRNVKLGFFLHSPFPSSSE
MEL03C018715.2 EAYVSANKLFFQKVVEVINPDDDYIWIHDYHLMVLPFLRRRFRNVKMGFFLHSPFPSSSE
MEL03C012010.2 QAYVSANKL FADKVM EIIINPEEDSVWVHDYHLMVLPFLRKRFRNVKLGFFLHSPFPSSSE
:.*.*.*.* :.*.*.*.*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

MEL03C013838.2 IYRTLPRVDELLRALLNSDLIGFHTFDYARHFLSCCSRMLGLSYQSKRGYIGLEYGRYV
MEL03C018715.2 IYRTLPRVEILKALLNSDIIGFHTFDYARHFLSCCSRMLGLEYSKRGYLGLEYGRYV
MEL03C012010.2 IYRTLPRVEILRGLNCDLLGFHTFDYARHFLSCCSRMLGLDYESKRGHIGLDYYGRV
*****:*:*:*.*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*

MEL03C013838.2 SIKILPVGIIHGQLQVNLNLPETVSKVAELQDRFGQTVLLGVDDMDIFKGISLKL LAFE
MEL03C018715.2 GIKIMPVGIHMSRIESVMKLADEDAKTRELTQQFAGKTVLLGVDDLDIFKGINLKL LAME
MEL03C012010.2 YIKILPVGIIHMGRLESVMNLPSTFAKVKIIRDQFMGKKLILGIDMDIFKGISLKL LAVE
***:*****:..:.*:*.*. *.* *:*:*:*:*:*:*:*:*:*:*:*:*:*:*

MEL03C013838.2 QLLRQHPERWGKAVLVQIANPARGRDKDQVEVAETTATVDRINTTFRPGYEPVVLINT
MEL03C018715.2 QVLKQHPKWIQKAVLIQIVNPARGGKRDQIEI EDEIKESCRRINKYGHGPGYEPVLLDR
MEL03C012010.2 QLLRQHPALRGKIVLVQIVNPARGGKDVHEAQKAYLAAERINEAYGSSNYKPVILDR
*:*:*.* ** *:*.*.* ***:.*:* * : ** : .*::*:*:*

MEL03C013838.2 PLQFYERIAYYAIAECCLVAVRDGMNLPYIYICRQGNEKLDLVLGLNPSAAKSMVLV
MEL03C018715.2 HVPITERVAYYSIAECVAVTAVRDGMNLPYIYVVCRXGNHLPKMFELQR--TKKSMVLV
MEL03C012010.2 PVPRFEKTAYYALAECCIVSAVRDGMNLPYKYIVCRQSTPLMDEALGLQIGSPRTSMVLV
: * : ***:*** *:*:*:*.* *:*:*.* .. : . * : . : ***

MEL03C013838.2 LSEFIGCSPSLSGAIRVNPWNIEAVTEAMDSALVIPEAEKQLRHEKHYRYVSTHDVAYWA
MEL03C018715.2 ISEFIGCSPSLSGAFRNPWNVEKTAELNEAISMADESKQLRHEKHYRYVATHDVAYWS
MEL03C012010.2 VSEFIGCSPSLSGAIRVNPWDIDAVADALELAI TMQSEKQLRHEKHYRYVSSHDIQYWS
:*****:*****:..:.*:*:* * : : :*****:*****:***:.*.*

MEL03C013838.2 RSFLQDLGRACRDHSMRRCWIGFGLGFRVIALDPDFRKLSDVHIVSVYKRTGYRALLD
MEL03C018715.2 RSFLQDMERTCSDHFRRCWIGFSGFRVVALDPNFRKLSDVAIVSSYSRAESRAILLD
MEL03C012010.2 RSFMQDLDRACQDHYSKRWCWIGLGLFRVVSLSPGFRKLTIDHIVSAYKRTHRAIFLD
**:*:*.* * * * :*****:..: **:*:*.*.* ***:.* * * * * * * * * * * *

MEL03C013838.2 YDGIIMTLPGSI SMNPTSEALGILNNLCKDPKNVFLVSGKDRKLTTEWTFSPCEKLGIAAE
MEL03C018715.2 YDGTVM PQNSINKSPSAQVISILNLT CADAKNVFIVSGRGRDSLKWF C PCKKLGIAAE
MEL03C012010.2 YDGTIISQSSIITPSPEVISVLTTL CNDP CNTVFIVSGRGRSSLGQWVFSCEMLGIAAE
** * : .** *.*:..:.*.* * * * * * * * * * * * * * * * * * * * * *

MEL03C013838.2 HGFYLRPNQTADWETCVAVTDFDWKQIAEPMQLYTETTDGSTIETKESALVWNLYADP
MEL03C018715.2 HGFYLRQSQNEEWKICGQSSDFGWMHIAEPMKLYTEATDGSSI ERKESALVWQYRDADP
MEL03C012010.2 HGFYIRWGGTSEWETSPSSDLWIKIVEPMRLYTEATDGSCIEQKESALVWHHQDADS
**:*:*.* ..:.*. *:*.* *:*.* *:*.* * * * * * * * * * * * * * * * * *

MEL03C013838.2 DFGSCQAKELLDHLESVLANEPVSVKSGQHIVEVKPQGVNKGIVAEYLLQTMKEKGMPLD
MEL03C018715.2 GFGSSQAKEMLDHLESVLANEPVAVKSGQFIVEVKPQGVTKGLVAEKIFSSMAEDGKLAD
MEL03C012010.2 DFGSCQAKELLDHLENLANEPVAVKRGQHIVEVKPQGVSKGLVAEKVLSRMVDSGRPPD
.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*

MEL03C013838.2 FVLCIGDDRSDEDMFEVIMNAKAS--LSPGAEVFGCTVGQKPSKARYLLEDTHEILRMLQ
MEL03C018715.2 FVLCIGDDRSDEDMFEIIGNALSNNILSPTTSVFACTVVGQKPSKAKYYLDDTAEVISMLE
MEL03C012010.2 FVMCIGDDRSDEDMFESILSTVSSPSLPSAPEIFACTVGRKPSKAKFYLLDDTSDVVKLLQ
**.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*.*

MEL03C013838.2 GLTHASEHATRAAPQTTARRVIAESK
MEL03C018715.2 YLAEASSPLSSDDEEGENAS-----
MEL03C012010.2 CLASSSRPRRQLPQMRVSFESVF---
*:*.* . :

```

Similarity results (<http://imed.med.ucm.es/Tools/sias.html> software)

```

MEL03C013838.2 100%
MEL03C018715.2 73.94%      100%
MEL03C012010.2 72.55%      70.67%     100%
MEL03C013838.2 MEL03C018715.2 MEL03C012010.2

```